Supplementary materials

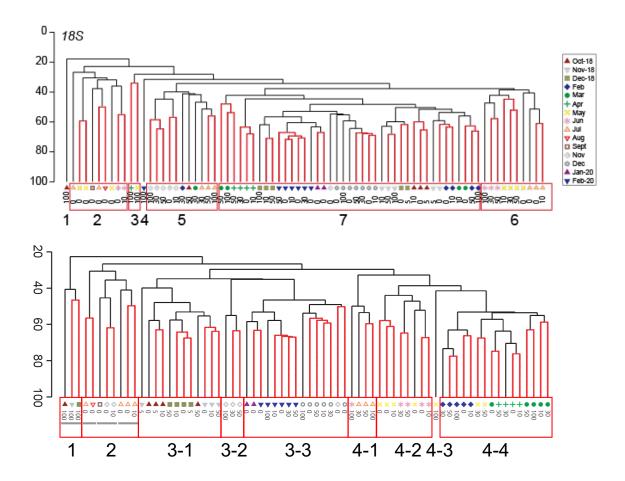


Figure S1 Cluster analysis results (group average) of eukaryotic (upper) and bacterial community (lower) in Sagami Bay. (A) Red lines represented results of SIMPROF test. (B) Each point represents each sample and different color represent each cluster.

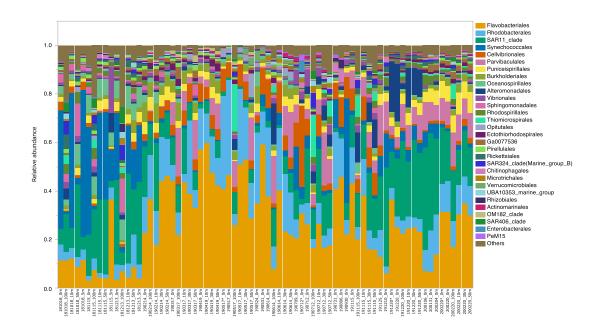


Figure S2 Taxonomic relative contributions to the bacterioplankton faction for each sample in Order level.

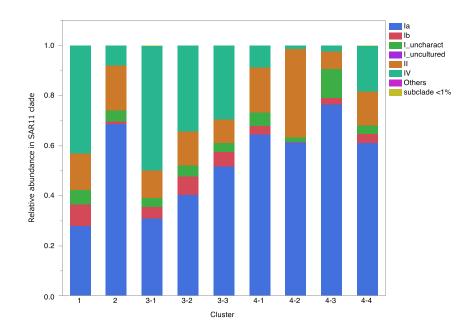


Figure S3 Relative abundance of SAR11 subclades in SAR11 clade in each cluster.

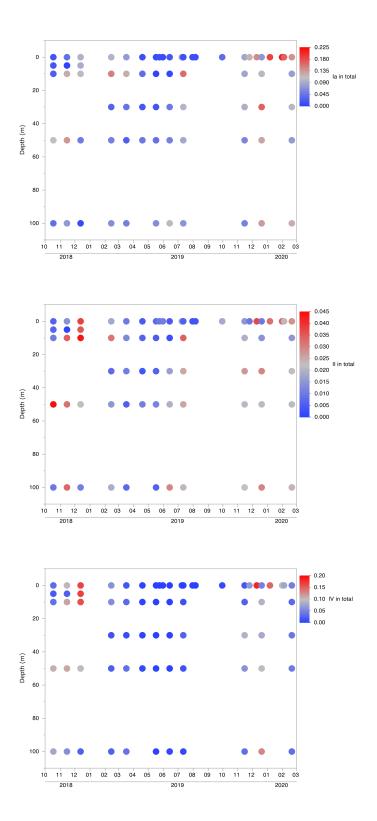


Figure S4 Spatiotemporal distributions of SAR11 subclades Ia, II and IV shown by their relative abundances in total bacterial community.

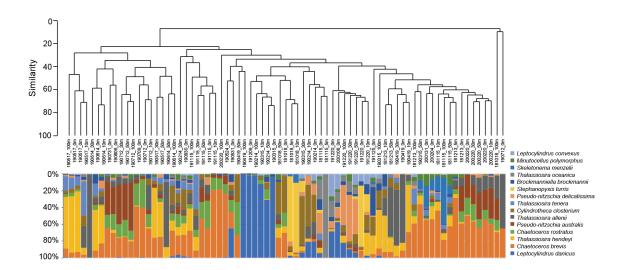


Figure S5 Cluster analysis of diatom and relative reads abundance of top 15 OTUs classified to species level.

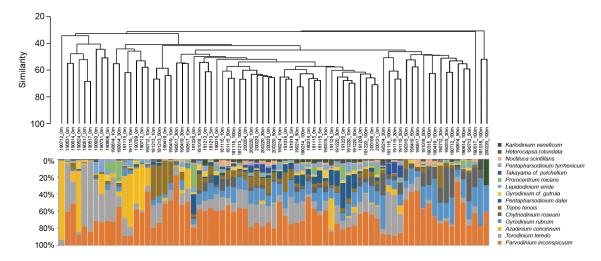


Figure S6 Cluster analysis of dinoflagellates and relative reads abundance of top 15 OTUs classified to species level.

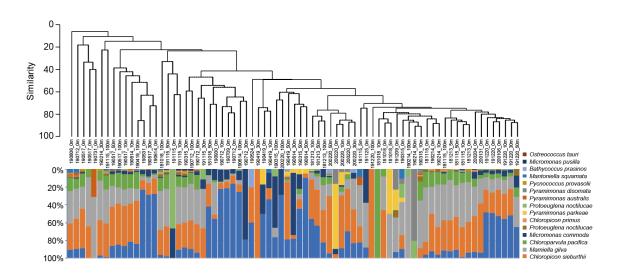


Figure S7 Cluster analysis of green algae and relative reads abundance of top 15 OTUs classified to species level.

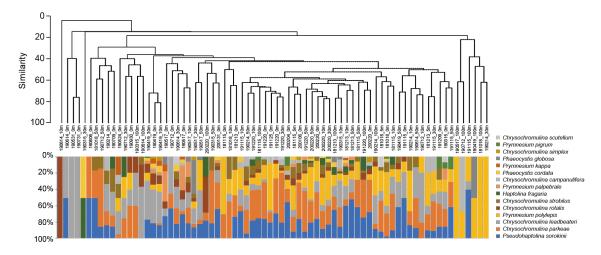


Figure S8 Cluster analysis of haptophytes and relative reads abundance of top 15 OTUs classified to species level.